Amendments to the Claims

Claim 1 (currently amended): An isolated and purified compound~~, said compound~~ having the structure of a human IgG binding pocket and comprising a first interacting surface, which is defined by the structure coordinates shown in Fig 1a for an IgG κ light chain for the amino acids Q124, S127, G128, T129, S131, V133, G157, N158, S159, Q160, E161, S162, S176, S177, T178, T180, and L181, and a second interacting surface, which is defined by the structure coordinates shown in Fig 1b for an IgG heavy chain for the amino acids P128, S129, L133, L150, K152, F175, P176, V178, L179, Q180, L184, L187 and S188, or a functional derivative of said compound.

Claim 2 (currently amended): ~~A compound according to~~ The compound of claim 1, wherein the second interacting surface is further defined by the structure coordinates shown in Fig 1 for an IgG heavy chain for the amino acids K126, F131, D153, S181, S182, and S186.

Claim 3 (currently amended): ~~A compound according to~~ The compound of claim 1 ~~or 2~~, wherein the functional derivative of the compound has a root mean square deviation from the backbone atoms of the binding pocket amino acids of not more than 2.0Å.

Claims 4-5 (cancelled)

Claim 6 (currently amended): An isolated and purified composite polypeptide consisting of one polypeptide ~~according to claim 4~~ consisting of a portion of a human IgG κ light chain starting at one of amino acids 93 to 110 and ending at one of amino acids 187 to 214 of human IgG κ light chain as set forth in SEQ ID NO:1 and one polypeptide ~~according to claim 5~~ consisting of a portion of a human IgG heavy chain starting at one of amino acids 106 to 128 and ending at one of amino acids 215 to 225 of human IgG light chain as set forth in SEQ ID NO:2.

Claim 7 (currently amended): A polypeptide ~~according to claim 6,~~ which comprises a binding pocket located between a first interacting surface, which is defined by the structure coordinates shown in Fig 1a for an IgG κ light chain for the amino acids Q124, S127, G128, T129, S131, V133, G157, N158, S159, Q160, E161, S162, S176, S177, T178, T180, and L181, and a second interacting surface, which is defined by the structure coordinates shown in Fig 1b for an IgG heavy chain for the amino acids P128, S129, L133, L150, K152, F175, P176, V178, L179, Q180, L184, L187 and S188.

Claim 8 (currently amended): ~~A~~ The polypeptide ~~according to~~ of claim 7, wherein the second interacting surface is further defined by the structure coordinates shown in Fig 1 for an IgG heavy chain for the amino acids K126, F131, D153, S181, S182, and S186.

Claim 9 (currently amended): A complex comprising a ligand directly linked to the binding pocket of a polypeptide according to claims 6 or 7 ~~any one of claims 4-8~~.

Claim 10 (currently amended): ~~A~~ The complex ~~according to~~ of claim 9, wherein the binding constant is at least 10^{-4} M.

Claim 11 (currently amended): ~~A~~ The complex ~~according to~~ of claim 9 ~~or 10~~, wherein the molecule is a detectable label.

Claim 12 (currently amended): A method for evaluating the potential or ability of a chemical entity to associate with a human κ-Fab constant part-comprising composition, which method comprises ~~to provide~~ providing a library of chemical entities and screening said library for ability to bind to the binding pocket of a polypeptide according to claims 6 or 7 ~~any one of claims 4-8~~.

Claim 13 (currently amended): ~~A~~ The method ~~according to claims~~ of claim 12, ~~which includes a further step of~~ further comprising testing a selection of the chemical entities that associate to said binding pocket by contacting them with a human κ-Fab constant part-comprising composition and grading said entities according to affinity.

Claim 14 (currently amended): A method for evaluating the potential or ability of a chemical entity to bind a human κ-Fab constant part-comprising composition, which method comprises a first step wherein computational means are employed to perform a fitting operation between the chemical entity and the binding pocket of a polypeptide according to claim 6 or 7 ~~any one of claims 4-8~~, and a second step wherein the results of said fitting operation are analysed to quantify the binding between the chemical entity and the binding pocket.

Claim 15 (currently amended): A method of identifying a potential ligand to a human κ-Fab constant part-comprising composition, which method comprises

(a) generating a three-dimensional structure of the binding pocket of a polypeptide according to claim 6 or 7 ~~any one of claims 4-8~~;

(b) employing said three-dimensional structure to design a candidate ligand;

(c) providing said candidate ligand;

(d) contacting the candidate ligand with a human κ-Fab constant part-comprising composition comprising said binding pocket to verify any binding; and, optionally,

(e) repeating steps (b)-(d).

Claim 16 (currently amended): A method for evaluating the potential or ability of a chemical entity to associate with a human κ-Fab constant part-comprising composition, which method comprises the steps of

(a) providing a virtual library of chemical entities;

(b) docking the chemical entities to the binding pocket of a polypeptide according to claim 6 or 7 ~~any one of claims 4-8~~;

(c) defining at least one query based on the results of the docking operation;

(d) screening all entities docked in step (b) while in the docked conformation with the query defined in step (c) for evaluating the potential or ability thereof to bind to the compound or binding pocket;

(e) inspection and, optionally, removal of redundancy; and

(f) providing one or more of the chemical entities that bound the binding pocket and experimentally testing their binding to a human κ-Fab constant part-comprising composition; and, if more than one chemical entity was tested,

(g) rating the affinities thereof to human κ-Fab constant part-comprising composition.

Claim 17 (currently amended): ~~A~~ The method ~~according to~~ of claim 16, wherein step (a) further comprises a subsequent step of filtering and removal of redundancy among the entities of the library provided.

Claim 18 (currently amended): ~~A~~ The method ~~according to~~ of claim 17 ~~or 18~~, wherein the results of the docking operation of step (b) are evaluated by visual inspection of the contact between the interacting surface of the binding pocket and the molecular surface(s).

Claims 19-22 (cancelled)

Claim 23 (currently amended): A computer for producing a three-dimensional representation of the binding pocket of a polypeptide according to claim 6 or 7 ~~any one of claims 4-8~~, which computer comprises

(i) a computer-readable data storage medium comprising a data storage material encoded with computer-readable data, wherein said data comprises the structure coordinates as shown in Fig 1 for an IgG κ light chain for the amino acids Q124, S127, G128, T129, S131, V133, G157, N158, S159, Q160, E161, S162, S176, S177, T178, T180, and L181 and the structure coordinates as shown in Fig 1 for an IgG heavy chain for the amino acids P128, S129, L133, L150, K152, F175, P176, V178, L179, Q180, L184, L187 and S188;

(ii) a working memory for storing instructions for processing said computer-readable data;

(iii) a central-processing unit coupled to said working memory and to said computer-readable data storage medium for processing said computer-machine readable data into said three-dimensional representation; and

(iv) a display coupled to said central-processing unit for displaying said three-dimensional representation.

Claim 24 (currently amended): ~~A~~ The computer ~~according to~~ of claim 23, wherein the computer-readable data further comprises the structure coordinates as shown in Fig 1 for an IgG heavy chain for the amino acids K126, F131, D153, S181, S182, and S186.

Claim 25 (currently amended): A machine-readable datastorage medium comprising a data storage material encoded with machine-readable data, wherein said data is defined by all or a portion of the structure coordinates of the binding pocket of a polypeptide according to claim 6 or 7 ~~any one of claims 4-8~~.